

OriGene Technologies, Inc.

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Product datasheet for PH309462

ATP6V1B1 (NM_001692) Human Mass Spec Standard

Product data:

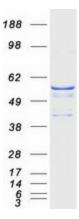
Product Type:	Mass Spec Standards
Description:	ATP6V1B1 MS Standard C13 and N15-labeled recombinant protein (NP_001683)
Species:	Human
Expression Host:	HEK293
Expression cDNA Clone or AA Sequence:	RC209462
Predicted MW:	56.8 kDa
Protein Sequence:	>RC209462 protein sequence <mark>Red</mark> =Cloning site Green=Tags(s)
	MAMEIDSRPGGLPGSSCNLGAAREHMQAVTRNYITHPRVTYRTVCSVNGPLVVLDRVKFAQYAEIVHFTL PDGTQRSGQVLEVAGTKAIVQVFEGTSGIDARKTTCEFTGDILRTPVSEDMLGRVFNGSGKPIDKGPVVM AEDFLDINGQPINPHSRIYPEEMIQTGISPIDVMNSIARGQKIPIFSAAGLPHNEIAAQICRQAGLVKKS KAVLDYHDDNFAIVFAAMGVNMETARFFKSDFEQNGTMGNVCLFLNLANDPTIERIITPRLALTTAEFLA YQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTDLATIYERAGRVEGRGGSITQIPILTM PNDDITHPIPDLTGFITEGQIYVDRQLHNRQIYPPINVLPSLSRLMKSAIGEGMTRKDHGDVSNQLYACY AIGKDVQAMKAVVGEEALTSEDLLYLEFLQKFEKNFINQGPYENRSVFESLDLGWKLLRIFPKEMLKRIP QAVIDEFYSREGALQDLAPDTAL
	TRTRPLEQKLISEEDLAANDILDYKDDDDKV
Tag:	C-Myc/DDK
Purity:	> 80% as determined by SDS-PAGE and Coomassie blue staining
Concentration:	>0.05 µg/µL as determined by microplate BCA method
Labeling Method:	Labeled with [U- 13C6, 15N4]-L-Arginine and [U- 13C6, 15N2]-L-Lysine
Buffer:	25 mM Tris-HCl, 100 mM glycine, pH 7.3
Storage:	Store at -80°C. Avoid repeated freeze-thaw cycles.
Stability:	Stable for 3 months from receipt of products under proper storage and handling conditions.
RefSeq:	<u>NP 001683</u>
RefSeq Size:	1956
RefSeq ORF:	1539



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	ATP6V1B1 (NM_001692) Human Mass Spec Standard – PH309462
Synonyms:	ATP6B1; DRTA2; RTA1B; VATB; VMA2; VPP3
Locus ID:	525
UniProt ID:	<u>P15313</u>
Cytogenetics:	2p13.3
Summary:	This gene encodes a component of vacuolar ATPase (V-ATPase), a multisubunit enzyme that mediates acidification of eukaryotic intracellular organelles. V-ATPase dependent organelle acidification is necessary for such intracellular processes as protein sorting, zymogen activation, receptor-mediated endocytosis, and synaptic vesicle proton gradient generation. V-ATPase is composed of a cytosolic V1 domain and a transmembrane V0 domain. The V1 domain consists of three A and three B subunits, two G subunits plus the C, D, E, F, and H subunits. The V1 domain contains the ATP catalytic site. The V0 domain consists of five different subunits: a, c, c', c'', and d. Additional isoforms of many of the V1 and V0 subunit proteins are encoded by multiple genes or alternatively spliced transcript variants. This encoded protein is one of two V1 domain B subunit isoforms and is found in the kidney. Mutations in this gene cause distal renal tubular acidosis associated with sensorineural deafness. [provided by RefSeq, Jul 2008]
Protein Families	: Druggable Genome
Protein Pathway	/s: Epithelial cell signaling in Helicobacter pylori infection, Metabolic pathways, Oxidative phosphorylation, Vibrio cholerae infection

Product images:



Coomassie blue staining of purified ATP6V1B1 protein (Cat# [TP309462]). The protein was produced from HEK293T cells transfected with ATP6V1B1 cDNA clone (Cat# [RC209462]) using MegaTran 2.0 (Cat# [TT210002]).

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